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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:15:02 ; Search time 12 Seconds
(without alignments)
224.663 Million cell updates/sec

Title: US-09-664-326-23

Perfect score: 368
Sequence: 1 LTYDCTESGMCLCEGSN.....PKQSHNDGFEEIPEYIQ 65

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	360	97.8	65 1 ITTH_HIRME	P01050 hirudo medi
2	353	95.9	65 1 ITTH_HIRME	P28506 hirudo medi
3	352	95.7	65 1 ITTH_HIRME	P28511 hirudo medi
4	350	95.1	65 1 ITTH_HIRME	P28503 hirudo medi
5	348	94.6	65 1 ITTH_HIRME	P28509 hirudo medi
6	348	94.6	65 1 ITTH_HIRME	P28508 hirudo medi
7	346	94.0	65 1 ITTH_HIRME	P28507 hirudo medi
8	345	93.8	65 1 ITTH_HIRME	P28510 hirudo medi
9	345	93.8	65 1 ITTH_HIRME	P28505 hirudo medi
10	343	93.2	65 1 ITTH_HIRME	P09945 hirudo medi
11	333	90.5	72 1 ITTH_HIRME	P09944 hirudo medi
12	315	85.6	66 1 ITTH_HIRME	P28501 hirudo medi
13	293	79.6	63 1 ITTH_HIRME	P81492 hirudinaria
14	249	67.7	63 1 ITTH_HIRME	P28512 hirudinaria
15	225	58.4	63 1 ITTH_HIRME	P28511 hirudinaria
16	173	47.0	62 1 ITTH_HIRME	P28502 hirudo medi
17	90	24.5	17 1 ITTH_HIRME	P28502 hirudo medi
18	68.5	18.6	1071 1 VATA_YEAST	P17255 saccharomyc
19	68	18.5	192 1 YADK_RHISN	P55423 plasmodium s
20	67	18.2	222 1 OS28_PLAGA	O92832 homo sapien
21	66.5	18.1	810 1 NEEL_HUMAN	O90937 brachydanio
22	66	17.9	1242 1 JAGI_BRARE	P57999 oryctolagus
23	66	17.9	5376 1 ZAN_MOUSE	O88799 mus musculu
24	65.5	17.8	2700 1 ZAN_HUMAN	O94433 homo sapien
25	65	17.7	306 1 C181_HUMAN	O15165 homo sapien
26	64	17.4	317 1 IBP2_SHEEP	O29400 ovis aries
27	63.5	17.3	318 1 GSHB_VIBCH	O90937 brachydanio
28	63.5	17.3	474 1 VSM5_TRYBB	P26333 trypanosoma
29	63.5	17.3	755 1 COMP_RAT	P35444 rattus norv
30	63.5	17.3	1218 1 JAGI_HUMAN	P78504 homo sapien
31	63.5	17.3	1218 1 JAGI_HUMAN	O90937 homo sapien
32	63.5	17.3	1218 1 JAGI_HUMAN	O90937 homo sapien
33	63.5	17.3	2703 1 NOTC_DROME	P07207 drosophila

34	63	17.1	80 1 AFP4_RAPSA	O24331 raphanus sa
35	63	17.1	385 1 GUNE_FUSOX	P46239 fusarium ox
36	62.5	17.0	513 1 AVR2_HUMAN	P27037 homo sapien
37	62	16.8	79 1 AFP3_BRANA	O39313 brassica na
38	62	16.8	79 1 AFP3_RAPSA	O24332 raphanus sa
39	62	16.8	80 1 AFP2_ARATH	O80955 arabidopsis
40	62	16.8	80 1 AFP3_ARATH	O80954 arabidopsis
41	62	16.8	80 1 AFP4_ARATH	O91123 arabidopsis
42	62	16.8	264 1 SPC2_MOUSE	P34714 caenorhabdi
43	62	16.8	2470 1 NTC2_MOUSE	O35516 mus musculu
44	62	16.8	2471 1 NTC2_HUMAN	O04721 homo sapien
45	62	16.8	2471 1 NTC2_RAT	O9q30 rattus norv

ALIGNMENTS

RESULT 1
ID ITTH_HIRME STANDARD; PRT; 65 AA.
AC P01050;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hirudin variant-1 (Lepridin).
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinae;
OC Arynchobdellidae; Hirudiniformes; Hirudinae; Hirudo.
NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RA Dotti J., Mueller H.-P., Seemuller U., Chang J.-Y.;
RT "The complete amino acid sequence of hirudin, a thrombin specific
inhibitor. Application of colour carboxymethylation.";
RL FEBS Lett. 165:180-183(1984).
RN [2]
RP SEQUENCE.
RA Petersen T.E., Roberts H.R., Sottrop-Jensen L., Magnusson S.,
RA Bagdy D.;
RL (in) Peeters H. (eds.);
RL "Proteins of the biological fluids, Proc. 23th colloquium, pp.145-149,
[3]
RP STRUCTURE BY NMR.
RX MEDLINE=89274194; PubMed=2567183;
RA Folkers P.J.M., Clore G.M., Driscoll P.C., Dotti J., Koehler S.,
RA Gronenborn A.M.;
RT "Solution structure of recombinant hirudin and the Lys-47-->Glu
mutant: a nuclear magnetic resonance and hybrid distance
geometry-dynamical simulated annealing study.";
RL Biochemistry 28:2601-2617(1989).
RN [4]
RP STRUCTURE BY NMR OF 1-51.
RX MEDLINE=93116062; PubMed=1335515;
RA Szyperski T., Guentert P., Stone S.R., Wuehrlich K.;
RT "Nuclear magnetic resonance solution structure of hirudin(1-51) and
comparison with corresponding three-dimensional structures determined
using the complete 65-residue hirudin polypeptide chain.";
RL J. Mol. Biol. 228:1193-1205(1992).
CC -I- FUNCTION. HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
THROMBIN. THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -I- PHARMACEUTICAL: Available under the name Refludan (Hoechst Marion
Roussel). Used to treat heparin-induced thrombocytopenia (HIT).
CC -I- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC -I- DATABASE: NAME=Refludan; NOTE=Clinical information on Refludan;
WWW="http://www.refludan.com/".
CC PIR; A01289; HDLXH.
DR PDB; 2HIR; 15-JAN-90.
DR PDB; 4HIR; 15-JAN-90.
DR PDB; 5HIR; 15-JAN-90.
DR PDB; 6HIR; 15-JAN-90.
DR PDB; 1HIC; 31-JAN-94.

DR PDB: 1HAG; 20-DEC-94.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family;
 KW Pharmaceutical; 3D-structure.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD.RES 63 63
 FT STRAND 5 5
 FT TURN 9 10
 FT STRAND 11 12
 FT STRAND 15 17
 FT TURN 18 19
 FT STRAND 20 21
 FT TURN 24 25
 FT STRAND 26 29
 FT STRAND 38 41
 FT STRAND 45 46
 SQ SEQUENCE 65 AA; 6970 MW; 9085A5876E3DE9FF CRC64;

Query Match 97.8%; Score 360; DB 1; Length 65;
 Best Local Similarity 96.9%; Pred. No. 2e-32;
 Matches 63; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 OY 61 EYLIQ 65
 |||||
 DB 61 EYLIQ 65

RESULT 2
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28506;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIB.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; Pubmed=2792365;
 RA Scharf M., Engels J., Tripler D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P09945; ATHTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD.RES 63 63
 SQ SEQUENCE 65 AA; 6985 MW; 8F7AEAE5EA30913 CRC64;

Query Match 95.9%; Score 353; DB 1; Length 65;

Best Local Similarity 93.8%; Pred. No. 1.1e-31;
 Matches 61; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 OY 61 EYLIQ 65
 |||||
 DB 61 EYLIQ 65

RESULT 3
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28511;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIB.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; Pubmed=2792365;
 RA Scharf M., Engels J., Tripler D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050; IHTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD.RES 63 63
 SQ SEQUENCE 65 AA; 6968 MW; 85FD9E1AE3DE9FF CRC64;

Query Match 95.7%; Score 352; DB 1; Length 65;
 Best Local Similarity 93.8%; Pred. No. 1.4e-31;
 Matches 61; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 OY 61 EYLIQ 65
 |||||
 DB 61 EYLIQ 65

RESULT 4
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28503;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIA.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=90005945; PubMed-2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR PIR; S05673; S05673.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR ProDom; PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUPFATON (BY SIMILARITY).
SQ SEQUENCE 65 AA; 6987 MW; 817E1541CF53C73 CRC64;

Query Match 95.1%; Score 350; DB 1; Length 65;
Best local Similarity 93.8%; Pred. No. 2, 3e-31;
Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTYDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
DB 1 IYTDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

QY 61 EYIQ 65
|||||
DB 61 EYIQ 65

RESULT 5

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28504;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin II.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxId=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed-2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR ProDom; PD004216; Hirudin; 1.

KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUPFATON (BY SIMILARITY).
SQ SEQUENCE 65 AA; 6986 MW; 757EAE35FAEB27E CRC64;

Query Match 94.6%; Score 348; DB 1; Length 65;
Best local Similarity 92.3%; Pred. No. 3, 8e-31;
Matches 60; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTYDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

DB 1 IYTDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
QY 61 EYIQ 65
|||||
DB 61 EYIQ 65

RESULT 6

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28509;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin II.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxId=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed-2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR PIR; S05676; S05676.
DR HSSP; P01050; 1HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR ProDom; PD004216; Hirudin; 1.

KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUPFATON (BY SIMILARITY).
SQ SEQUENCE 65 AA; 7027 MW; 05E6F176E3DE9FC CRC64;

Query Match 94.6%; Score 348; DB 1; Length 65;
Best local Similarity 93.8%; Pred. No. 3, 8e-31;
Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTYDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
DB 1 VYTDCTESGONLCLCGSNVCGGKNCILGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

QY 61 EYIQ 65
|||||
DB 61 EYIQ 65

RESULT 7

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28308;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin IIa.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxId=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed-2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR ProDom; PD004216; Hirudin; 1.

RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050.1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR ProDom: PD004216; Hirudin; 1.
 DR KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 6973 MW; CABBR0D72B6449B4 CRC64;

Query Match . 94.0%; Score 346; DB 1; Length 65;
 Best Local Similarity 90.8%; Pred. No. 6.3e-31;
 Matches 59; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVYVCTESGQNLCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 : |||||
 DB 1 VYVTCESGEGDLCCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 OY 61 EYELQ 65
 |||||
 DB 61 EYELQ 65

RESULT 8
 ITHG_HIRME STANDARD; PRT; 65 AA.
 ID ITHG_HIRME
 AC P28507;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIa.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050.1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR ProDom: PD004216; Hirudin; 1.
 DR KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7028 MW; 05F6A0B26A3DE9FC CRC64;

Query Match . 93.8%; Score 345; DB 1; Length 65;
 Best Local Similarity 92.3%; Pred. No. 8e-31;
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVYVCTESGQNLCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 : |||||
 DB 1 VYVTCESGQNLCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 OY 61 EYELQ 65
 |||||
 DB 61 EYELQ 65

OY 61 EYELQ 65
 |||||
 DB 61 EYELQ 65

RESULT 9
 ITHG_HIRME STANDARD; PRT; 65 AA.
 ID ITHG_HIRME
 AC P28510;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIb.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050.1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR ProDom: PD004216; Hirudin; 1.
 DR KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7026 MW; 1E902A81AE3DE9FC CRC64;

Query Match . 93.8%; Score 345; DB 1; Length 65;
 Best Local Similarity 92.3%; Pred. No. 8e-31;
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVYVCTESGQNLCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 : |||||
 DB 1 VYVTCESGQNLCEGSSNVCGGCKILGSDGKKNOCVTGEGTPKQSHNDGDFEELP 60
 OY 61 EYELQ 65
 |||||
 DB 61 EYELQ 65

RESULT 10
 ITHG_HIRME STANDARD; PRT; 65 AA.
 ID ITHG_HIRME
 AC P28505;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin II'.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-

Db	61	ED	62
RESULT 13			
ITHA_HIRME	ITHA_HIRME	STANDARD:	PRT: 65 AA.
ID	P28501;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hirudin I (Fragments).		
OS	Hirudo medicinalis (Medicinal leech).		
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;		
OC	Atrichobdellida; Hirudiniformes; Hirudinidae; Hirudo.		
OX	NCBI_Taxid=6421;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=90005945; PubMed=2792365;		
RA	Scharf M., Engels J., Tripler D.;		
RT	"Primary structures of new 'iso-hirudins'.";		
RL	FEBS Lett. 255:105-110(1989).		
CC	-1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE		
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-		
CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.		
CC	-1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.		
DR	HSP; S05672, S05672.		
DR	HSP; P01050; HHC.		
DR	InterPro; IPR000429; Hirudin.		
DR	Pfam; PF00713; Hirudin; 1.		
DR	PRINTS; PR00777; HIRUDIN.		
DR	ProDom; PD004216; Hirudin; 1.		
KW	Serine protease inhibitor; Sulfation; Multigene family.		
FT	DISULFID 6 14		
FT	DISULFID 16 28		
FT	DISULFID 22 39		
FT	MOD_RES 63 63		
SQ	SEQUENCE 65 AA; 7126 MW; B79C5A9D11677AD5 CRC64;		
Query Match 79.6%; Score 293; DB 1; Length 65;			
Best Local Similarity 81.5%; Pred. No. 3.2e-25;			
Matches 53; Conservative 1; Mismatches 11; Indels 0; Gaps 0;			
QY	1	LYTDDCTSSGNCILCESSNVCNGGKNKILGSDGKNCVYGEPTPKQSHNDGDFEIP	60
Db	1	VVYDCTSSGNCILCEXXXXXXXKXCLGSDGKNCVYGEPTPKQSHNDGDFEIP	60
QY	61	EYLLD 65	
Db	61	EYLLD 65	
RESULT 14			
ITHV_HIRMA	ITHV_HIRMA	STANDARD:	PRT: 63 AA.
ID	P81492;		
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-DEC-1998 (Rel. 37, Last annotation update)		
DE	Hirudin HVI (Bufurudin).		
OS	Hirudinaia manillensis (Buffalo leech).		
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;		
OC	Atrichobdellida; Hirudiniformes; Hirudinidae; Hirudinea.		
OX	NCBI_Taxid=6419;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Head;		
RX	MEDLINE=94000343; PubMed=6397794;		
RA	Electricwala A., Hartwell R., Scawen M.D., Atkinson T.;		
RT	"The complete amino acid sequence of a hirudin variant from the leech		
RT	Hirudinaia manillensis.";		
RL	J. Protein Chem. 12:365-370(1993).		
CC	-1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE		
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-		

CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
DR	-I- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC	HSSP; P01050; SHR.
DR	InterPro; IPR000429; Hirudin.
DR	Pfam; PF00713; Hirudin; 1.
DR	PRINTS; PR00777; HIRUDIN.
DR	Produm; PD004216; Hirudin; 1.
KW	Serine protease inhibitor; Multigene family.
FT	DISULFID 6 14
FT	16 28 BY SIMILARITY.
FT	DISULFID 22 37 BY SIMILARITY.
SO	SEQUENCE 63 AA; 6699 MW; 8BC282B85C51BED CRC64;
OY	Query Match 67.7%; Score 249; DB 1; Length 63; Best Local Similarity 67.7%; Pred. No. 1.7e-20; Matches 44; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
Dd	1 LTYDCTESGNYCLCVSNVCGGNKCIIGSDGKNOCVTGEPTPKPSHNDGPFEETP 60 1 VSYDCTESGNYCLCVSNVCGEKNKLSSSG--NOCVMGEITPKRSQTEGDPEETP 58
OY	61 EHYLO 65 : : Db 59 DEXIK 63
RESULT 15	
ID	ITH6_HIRMA STANDARD; PROT; 63 AA.
AC	P28512:
DT	01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hirudin p6.
OS	Hirudinarria manillensis (Buffalo leech).
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinae;
CC	Arynchobdellidae; Hirudiniiformes; Hirudindidae; Hirudinarria.
OX	NCBI_Taxid=6419;
RN	[1]
RP	SEQUENCE, AND STRUCTURE OF CARBOHYDRATE.
RX	MEDLINE=92172851; Pubmed=1540584;
RA	Steiner V., Knecht R., Boersen O., Gassmann E., Stone S.R.,
RA	Rachdorf F., Schlaeppl J.-M., Maschler R.;
RT	"Primary structure and function of novel O-glycosylated hirudins from
RL	the leech Hirudinarria manillensis.";
Biochemistry	31:2294-2298(1992).
CC	-I- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC	-I- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC	-I- PWM: O-LINKED GLYCAN CONSISTS OF FUC-GAL-GALNAc TRISCHARIDE.
DR	PIR; A42207; A42207.
DR	HSSP; P01050; SHR.
DR	GlycoSuiteDB; P28512; -
DR	InterPro; IPR000429; Hirudin.
DR	Pfam; PF00713; Hirudin; 1.
DR	PRINTS; PR00777; HIRUDIN.
DR	Produm; PD004216; Hirudin; 1.
KW	Serine protease inhibitor; Sulfation; Glycoprotein;
FT	DISULFID 6 14 BY SIMILARITY.
FT	DISULFID 16 28 BY SIMILARITY.
FT	DISULFID 22 37 BY SIMILARITY.
FT	CARBOHYD 43 43 O-LINKED (GALNAc . .).
FT	/FTTD-CAR 000143.
SO	MOD_RES 61 61 SUITATION (BY SIMILARITY). SEQUENCE 63 AA; 6977 MW; 1A9A7369CC75A192 CRC64;
OY	Query Match 58.4%; Score 215; DB 1; Length 63; Best Local Similarity 60.9%; Pred. No. 7.6e-17; Matches 39; Conservative 7; Mismatches 16; Indels 2; Gaps 1;
1	LTYDCTESGNYCLCVSNVCGGNKCIIGSDGKNOCVTGEPTPKPSHNDGPFEETP 60

Db	1	MRTACTESQONOCICGNDVCGGRCQFPDSSGK--CVEGETRKPONEGQHDDPIP	58
OY	61	EEXL 64	
Db	59	EEXL 62	

Search completed: December 30, 2002, 16:17:00
job time : 13 secs

